



TITLE:

Gene expression of nutrient-sensing molecules in I cells of CCK reporter male mice

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1 **Gene expression of nutrient-sensing molecules**

2 **in I cells of CCK reporter male mice**

3

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15

16 **Short title:** Gene expression in I cell of CCK reporter mice

17

18 **Key words:** cholecystikinin, I cell, free fatty acid receptor, glucose transporter, peptide

19 receptor

20

21 4041 words

22 **Abbreviations:**

23 CCK: Cholecystokinin

24 GIP: Glucose-dependent insulintropic polypeptide / gastric inhibitory polypeptide

25 GLP-1: Glucagon-like peptide-1

26 FFAR: Free fatty acid receptor

27 GPR: G protein-coupled receptor

28 FATP: Fatty acid transport protein

29 CD36: Cluster of differentiation 36

30 SGLT1: Sodium-glucose cotransporter 1

31 GLUT: Glucose transporter

32 TGR5: Transmembrane GPR 5

33 PEPT1: Peptide transporter 1

34 CASR: Calcium-sensing receptor

35

36 **Abstract**

37 Cholecystinin (CCK) is secreted from enteroendocrine I cells in response to fat,
38 carbohydrate, and protein ingestion. Gene expression of nutrient-sensing molecules in I
39 cells remains unclear, primarily due to the difficulty in distinguishing I cells from intestinal
40 epithelial cells *in vivo*. In this study, we generated CCK reporter male mice in which the red
41 fluorescence protein tdTomato (Tomato) is produced by activation of the native murine *Cck*
42 promoter. Fluorescence microscopy revealed the presence of Tomato-positive cells in
43 upper small intestine (SI), lower SI, and colon. Flow cytometer analysis revealed that
44 Tomato-positive cells among epithelial cells of upper SI, lower SI, and colon occurred at the
45 rate of 0.95%, 0.54%, and 0.06%, respectively. In upper SI and lower SI, expression levels of
46 *Cck* mRNA were higher in Tomato-positive cells than those in Tomato-negative cells. The
47 fatty acid receptors *Gpr120*, *Gpr40*, and *Gpr43* and the oleoylethanolamide receptor
48 *Gpr119* were highly expressed in Tomato-positive cells isolated from SI, but were not found
49 in Tomato-positive cells from colon. The glucose and fructose transporters *Sglt1*, *Glut2*, and
50 *Glut5* were expressed in both Tomato-positive cells and -negative cells, but these
51 expression levels tended to be decreased in Tomato-positive cells from upper SI to colon.
52 The peptide transporter *Pept1* and receptor *Gpr93* were expressed in both Tomato-positive
53 cells and -negative cells, whereas *Casr* was expressed only in Tomato-positive cells isolated
54 from SI. Thus, this transgenic mouse reveals that I cell number and gene expression in I cells
55 vary according to region in the gastrointestinal tract.

56

57 Introduction

58 Gut hormones are released from enteroendocrine cells in response to nutrients, and
59 play an important role in food intake, nutrient absorption, energy accumulation and glucose
60 homeostasis. For example, ghrelin secreted from X/A-like cells expressed in the stomach
61 increases food intake and body weight (Nakazato *et al.* 2001); peptide YY (PYY) and the
62 incretin glucagon-like peptide-1 (GLP-1) released from enteroendocrine L cells inhibit food
63 intake and reduce body weight (Davis *et al.* 1998, Batterham *et al.* 2002). In addition,
64 glucose-dependent insulinotropic polypeptide / gastric inhibitory polypeptide (GIP) is an
65 incretin secreted from enteroendocrine K cells, and plays an important role in obesity and
66 insulin resistance under high-fat diet (HFD)-fed condition (Harada *et al.* 2008, Nasteska *et*
67 *al.* 2014, Joo *et al.* 2017, Shimazu-Kuwahara *et al.* 2017).

68 Cholecystokinin (CCK) is a gut hormone secreted from enteroendocrine I cells in small
69 intestine and colon (Fakhry *et al.* 2017), and activates the nucleus of the solitary tract
70 through the vagus nerve system to suppress appetite and food intake (Whited *et al.* 2006).
71 CCK-producing cells are expressed in the central nervous system, and directly inhibit food
72 intake (D'Agostino *et al.* 2016). The OLETF rat, which has a deletion in the *CCK1 receptor*
73 gene, shows hyperphagia and obesity (Otsuki *et al.* 1995, Tachibana *et al.* 1996). On the
74 other hand, CCK induces secretion of bile and pancreatic lipase, which are involved in fat
75 digestion and absorption (Rehfeld 2004). HFD-fed *Cck*-knockout mice demonstrate that
76 inhibition of CCK signaling alleviates body weight gain and insulin resistance under HFD-fed
77 condition (Lo *et al.* 2011). We previously reported that CCK has an important role in oil-

78 induced secretion of GIP, which is involved in body weight gain and insulin resistance
79 (Sankoda *et al.* 2017). This finding shows that CCK is involved in obesity and insulin
80 resistance under HFD-fed condition. Thus, regulation of CCK signaling or CCK secretion is a
81 potential therapeutic target for obesity and insulin resistance.

82 CCK is secreted from I cells by nutrient ingestion; fat and protein strongly stimulate
83 CCK secretion in comparison with glucose (Green *et al.* 1989, Pilichiewicz *et al.* 2007,
84 Hutchison *et al.* 2015). Some nutrient-sensing molecules have been identified. Glucose
85 transporters such as sodium-glucose cotransporter 1 (SGLT1) and glucose transporter 2
86 (GLUT2) are associated with GLP-1 and GIP secretion after glucose loading (Mace *et al.* 2012,
87 Gorboulev *et al.* 2012). Furthermore, free fatty acid receptors (FFARs) and fatty acid
88 transporters (FATPs) play an important role in free fatty acid sensing in gut hormone-
89 producing cells (Poreba *et al.* 2012, Lu *et al.* 2018). Some amino acid transporters and
90 receptors are involved in GLP-1 secretion (Diakogiannaki *et al.* 2013). In contrast, it remains
91 unclear whether these molecules are expressed in I cells, primarily due to the difficulty in
92 isolating them from intestinal epithelial cells. In this study, we generated CCK reporter male
93 mice in which the red fluorescence protein (RFP) variant tdTomato (Tomato) as well as CCK
94 is produced by activation of the native murine *Cck* promoter, and evaluated gene expression
95 of the molecules associated with nutrient sensing in I cells expressed in the gastrointestinal
96 (GI) tract.

97

98 **Materials and Methods**

99 **Animals**

100 *CCK-internal ribosome entry site (IRES)-Cre* knock-in (CCK-Cre) mice and Ai14 mice were
101 previously generated (JAX stock #012706, #007908) (Jackson Laboratory, Bar Harbor, Maine,
102 US) (Madisen *et al.* 2010, Taniguchi *et al.* 2011). CCK-Cre and Ai14 heterozygous (CCK-
103 Tomato) mice, which enabled visualization of I cells by Tomato fluorescence, were
104 generated by crossbreeding CCK-Cre homozygous mice and Ai14 homozygous mice. Ai14
105 heterozygous mice were used as control. Male mice at 8-13 weeks of age were used in flow
106 cytometer analysis and immunohistochemical analysis. We performed two cohorts to
107 evaluate the phenotype of CCK-Tomato mice. In one cohort, 8-week-old male mice were
108 weighed weekly for 20 weeks. Non-fasting blood samples were collected from the portal
109 vein of mice at 10 weeks of age, and plasma CCK concentrations were measured by CCK
110 fluorescent enzyme immunoassay (EIA) kit (FEK-069-04) (Phoenix Pharmaceuticals Inc.,
111 Burlingame, CA, US). In the other cohort, male mice at 19 weeks of age were used. Oral
112 glucose tolerance tests (OGTTs) and oral corn oil tolerance tests (OCTTs) were performed
113 after a 16-hour fasting period. Mice were administrated glucose of 6g/kg body weight for
114 OGTTs and corn oil of 10mL/kg body weight for OCTTs. Blood glucose levels were measured
115 at 0, 15 (for OGTTs), 30, 60, and 120 minutes after oral glucose or oil administration by the
116 glucose oxidase method (Sanwa Kagaku Kenkyusho, Nagoya, Japan). 60 μ l blood samples
117 were collected from peripheral blood vessels at 15 or 30 minutes after oral glucose or oil
118 administration, and plasma insulin (Shibayagi, Shibukawa, Japan) and CCK levels (Phoenix
119 Pharmaceuticals Inc.) were measured by EIA kit, respectively. Energy expenditure and

120 locomotor activity were measured by ARCO 2000 (ARCO System, Chiba, Japan) every 5
121 minutes over 24 hours with free access to water and diet (Kanemaru *et al.* 2020). Animal
122 care and procedures were approved by Kyoto University Animal Care Committee
123 (MedKyo15298).

124

125 ***Immunohistochemistry***

126 Stomach, upper small intestine (upper SI), lower small intestine (lower SI), and colon were
127 collected from CCK-Tomato mice and fixed by 4% paraformaldehyde. The protocol of
128 immunohistochemistry was previously described (Ikeguchi *et al.* 2018). Anti-CCK antibody
129 (CCK8-MO-167-2, 1:1000) (Frontier Institute Co., Ltd., Hokkaido, Japan), anti-RFP antibody
130 (600-401-379, 1:1000) (Rockland Immunochemicals Inc., Limerick, PA, US), and secondary
131 antibodies (Abcam, Cambridge, UK) were used. Images were taken using a fluorescence
132 microscope FSX100 (Olympus Corporation, Tokyo, Japan).

133

134 ***Isolation of Tomato-positive and -negative cells by flow cytometry***

135 The protocol to isolate fluorescence protein-producing cells from murine intestinal
136 epithelium was described previously (Suzuki *et al.* 2013). The small intestine was divided in
137 half, and the oral and rectal portions were defined as upper SI and lower SI, respectively.
138 The collected intestinal epithelial cells were filtered through a 40 μ m cell strainer (Becton,
139 Dickinson and Company, Franklin Lakes, NJ, US), and phosphate buffered salts (PBS)
140 containing 4', 6-diamidino-2-phenylindole (DAPI) (Dojindo Molecular Technologies, Inc.,

141 Kumamoto, Japan) was added. After excluding DAPI-positive cells as dead cells or doublets,
142 Tomato-positive cells and -negative cells were collected using FACS Aria III cell sorter
143 (Becton, Dickinson and Company). The number of Tomato-positive cells was also calculated
144 as Tomato-positive cells / intestinal epithelial cells (%).

145

146 **Quantitative reverse-transcription polymerase chain reaction (RT-PCR)**

147 Total RNAs of sorted Tomato-positive and -negative cells were extracted with a PicoPure
148 RNA Isolation Kit (Applied Biosystems, California, CA, US). For cDNA synthesis of sorted
149 2,000 Tomato-positive and -negative cells, RNA was reverse-transcribed using SuperScript
150 II Reverse Transcriptase and Oligo(dT)12-18 (Invitrogen, Carlsbad, CA, US). SYBR Green PCR
151 Master Mix (Applied Biosystems) was prepared for the PCR run. The mRNA expression levels
152 were measured by quantitative real-time PCR using the ABI PRISM 7000 Sequence
153 Detection System (Applied Biosystems). *Ppia* was used as the internal control. Each data
154 point was analyzed by the comparative threshold cycle method ($\Delta\Delta C_t$ method). Primer pairs
155 designed for evaluation of gene expression are as follows: *Glut2*, 5'-
156 AATGGTCGCCTCATTCTTTG-3' and 5'-ATCAAGAGGGCTCCAGTCAA-3'; *Glut5*, 5'-
157 TCATCTCTGTGTGGAAGTTG-3' and 5'-AGATCTGATCGGCGTAGTAG-3'; *Sglt1*, 5'-
158 GTGCTGGGCTGGATATTTGT-3' and 5'-AGGCCCAAGGCTAGATTGAT-3'; *Pept1*, 5'-
159 ATCATTGTGCTCATCGTGGC-3' and 5'-GTGCTTCAATCTCTGCTGGG-3'; *Gpr93*, 5'-
160 GGTGCTGATGATAATGGTGCT-3' and 5'-GTAGCCAAAGGCCTGGTATTC-3'; *Casr*, 5'-
161 GCATCAGGTATAACTCCGTGG-3' and 5'-TTGGAGACGGTGTTACAGGTG-3'; *Gpr41*, 5'-

162 TTCTTGCAGCCACACTGCTC-3' and 5'-GCCCACCACATGGGACATAT-3'; *Gpr43*, 5'-
 163 ACAGTGGAGGGGACCAAGAT-3' and 5'-GGGGACTCTCTACTCGGTGA-3'; *Gpr40*, 5'-
 164 TTTGCGCTGGGCTTTCC-3' and 5'-GCTGGGAGTGAGTCGCAGTT-3'; *Gpr119*, 5'-
 165 AGAAAGCGCCTATCACATCG-3' and 5'-CAACCTGCCTTTACCAGTTG-3'; *Cd36*, 5'-
 166 CGCTTTCTGCGTATCGTCTG-3' and 5'-GATGCACGGGATCGTGTCT-3'; *Fatp1*, 5'-
 167 TCTGTTCTGATTCGTGTTCGG-3' and 5'-AAGATGCACGGGATCGTGTC-3'; *Fatp2*, 5'-
 168 TCCTCCAAGATGTGCGGTACT-3' and 5'-TAGGTGAGCGTCTCGTCTCG-3'; *Fatp3*, 5'-
 169 ATGACAGGGGAGCCTATTCG-3' and 5'-ATCCTTCAGCAGCTTGCCT-3'; *Fatp4*, 5'-
 170 ACTGTTCTCCAAGCTAGTGCT-3' and 5'-GATGAAGACCCGGATGAAACG-3'; *Fatp5*, 5'-
 171 CTACGCTGGCTGCATATAGATG-3' and 5'-CCACAAAGGTCTCTGGAGGAT-3', *Secretin*,
 172 5'-AGCCCTTAGAGGACCAGCTC-3' and 5'-TGAACGATCAACAGCAGACC-3', *Glp-1*, 5'-
 173 TGAAGACAAACGCCACTCAC-3' and 5'-TCATGACGTTTGGCAATGTT-3'. Others were
 174 previously designed (Iwasaki *et al.* 2015, Sankoda *et al.* 2017).
 175

176 **Statistical analysis**

177 Results are shown as dot plot or mean \pm SEM. One or two data points of some results that
 178 exceeded mean \pm 2SD were excluded. Statistical significance was determined by Student's
 179 t-test or one way analysis of variance with Tukey or Games-Howell test. *P* values < 0.05 were
 180 considered statistically significant.

181

182 **Results**

183 ***Phenotype of CCK-Tomato mice***

184 IRES and Cre recombinase were inserted downstream of the murine *CCK* locus in CCK-
 185 Cre mice (Taniguchi *et al.* 2011). With this construction, the promoter and coding region of
 186 both *Cck* genes were intact in CCK-Tomato mice. Body weight of the CCK-Tomato mice was
 187 similar to that of control mice during 9-29 weeks of age (Fig. 1A). There was no significant
 188 difference in non-fasting CCK levels between control and CCK-Tomato mice (Control mice
 189 194.9 ± 102.1 mg/dl vs. CCK-Tomato mice 328.1 ± 248.1 mg/dl; $P=0.10$). There was no
 190 significant difference in food intake, energy expenditure and locomotor activity between
 191 CCK-Tomato mice and control mice (Fig. 1B and 1C). During OGTTs and OCTTs, blood glucose
 192 levels were not different between the two types of mice (Fig. 1D and 1E). Plasma insulin and
 193 CCK levels after glucose or corn oil administration were not different between the two
 194 groups. These results indicated that the *CCK-IRES-Cre* allele does not affect body weight gain,
 195 food intake, energy expenditure, locomotor activity, and glucose tolerance under 11% fat-
 196 containing diet-fed condition.

197

198 ***Number of I cells in CCK-Tomato mice***

199 Under fluorescence microscopy, Tomato-positive cells were detected in upper SI,
 200 lower SI, and colon of CCK-Tomato mice, but not in stomach (data not shown).
 201 Immunohistochemical analysis showed that Tomato-expressing cells were identical to CCK-
 202 expressing cells in upper SI, lower SI, and colon of CCK-Tomato mice (Fig. 2A).

203 We then evaluated the number of Tomato-expressing cells in small intestine and
 204 colon by histological analysis. The length of villus and the number of Tomato-expressing
 205 cells in small intestine were greater than those in colon (Fig. 2B and 2C). The ratio of
 206 Tomato-expressing cell number / length of villus was significantly higher in upper SI and
 207 lower SI than that in colon (Fig. 2D). In addition, the number of Tomato-positive cells was
 208 calculated by flow cytometry system (Fig. 2E). Tomato-positive cells / epithelial cells in
 209 upper SI, lower SI, and colon was $0.95 \pm 0.30\%$, $0.54 \pm 0.14\%$, and $0.06 \pm 0.01\%$, respectively.
 210 Tomato-positive cell number was greater in upper SI and lower SI than that in colon, but
 211 the number significantly differed only between lower SI and colon. After purification of each
 212 2,000 Tomato-positive and -negative cells, gene expression of *Cck* mRNA in the cells was
 213 evaluated (Fig. 2F). In upper SI, lower SI and colon, *Cck* mRNA expression was detected in
 214 Tomato-positive cells but not in Tomato-negative cells. In upper SI and lower SI, expression
 215 levels of *Cck* mRNA were higher in Tomato-positive cells than those in Tomato-negative cells.
 216 On the other hand, there was no significant difference in *Cck* mRNA expression levels
 217 between Tomato-positive and -negative cells in colon. *Cck* mRNA expression levels in
 218 Tomato-positive cells of upper SI and lower SI were significantly higher than those of colon.

219

220 ***Gene expression of molecules involved in fatty acid sensing in I cells***

221 We then evaluated gene expression of G protein-coupled receptors (GPRs) and
 222 transporters for free fatty acid. In upper SI and lower SI, expression levels of the long-chain
 223 fatty acid (LCFA) receptors *Ffar4* (*Gpr120*) (Fig. 3A) and *Ffar1* (*Gpr40*) (Fig. 3B) and the

224 oleoylethanolamide (OEA) receptor *Gpr119* (Fig. 3C) mRNA were significantly higher in
 225 Tomato-positive cells than those in Tomato-negative cells. The expression levels did not
 226 differ between Tomato-positive and -negative cells in colon. In upper and lower SI,
 227 expression levels of the short-chain fatty acid (SCFA) receptor *Ffar2* (*Gpr43*) mRNA (Fig. 3D)
 228 were high in Tomato-positive cells compared to those in Tomato-negative cells, but
 229 expression levels of *Ffar3* (*Gpr41*) mRNA (Fig. 3E) did not differ between Tomato-positive
 230 and -negative cells. *Bile acid receptor transmembrane GPR 5* (*Tgr5*) mRNA was highly
 231 expressed in Tomato-positive cells compared to that in Tomato-negative cells in lower SI
 232 (Fig. 3F). Gene expression of the fatty acid transport protein (FATP) 1-5 and cluster of
 233 differentiation 36 (CD36) was also evaluated. *Fatp4* and *Cd36* mRNA expressions were
 234 detected in Tomato-positive cells, but the expression levels did not differ between Tomato-
 235 positive cells and -negative cells (data not shown). *Fatp1*, *Fatp2*, *Fatp3*, and *Fatp5*
 236 expressions were not detected in Tomato-positive or -negative cells (data not shown).

237

238 ***Gene expression of molecules involved in glucose, fructose, and amino acid sensing in I***
 239 ***cells***

240 In upper SI, expression levels of glucose transporters *Sglt1* (Fig. 4A) and *Glut2* (Fig.
 241 4B) and fructose transporter *Glut5* (Fig. 4C) mRNA tended to be higher in Tomato-positive
 242 cells than those in Tomato-negative cells, but there was not a significant difference between
 243 the two groups. Expression levels of *Sglt1*, *Glut2*, and *Glut5* mRNA tended to be higher in

244 upper SI than those in lower SI. In colon, these expressions were not detected in Tomato-
245 positive cells.

246 Gene expression levels of *peptide transporter 1 (Pept1)* (Fig. 4D) and *Gpr93* (Fig. 4E),
247 which are protein metabolite-sensing molecules, did not differ between Tomato-positive
248 and -negative cells in upper and lower SI. In colon, *Gpr93* mRNA was not detected in
249 Tomato-positive or -negative cells, whereas *Pept1* mRNA was highly expressed in Tomato-
250 negative cells compared to that in Tomato-positive cells. mRNA of the *calcium-sensing*
251 *receptor (Casr)*, which is reported to be involved in amino acid-induced gut hormone
252 secretion (Mace *et al.* 2012), was highly expressed in Tomato-positive cells of upper SI (Fig.
253 4F). On the other hand, *Casr* mRNA was not detected in Tomato-negative cells.

254

255 ***Gene expression of gut hormones in I cells***

256 Some gut hormones are reported to be co-expressed in enteroendocrine cells (Egerod
257 *et al* 2012, Habib *et al* 2012). In addition, nutrient-sensing molecules are reported to be
258 expressed in glucose-dependent insulintropic polypeptide / gastric inhibitory polypeptide
259 (GIP)-producing K cells and glucagon-like peptide-1 (GLP-1)-producing L cells and to be
260 involved in nutrient-induced GIP and GLP-1 secretion (Iwasaki *et al* 2015, Reimann *et al*
261 2012). We therefore evaluated mRNA expression of other gut hormones in Tomato-positive
262 cells and -negative cells. *Secretin* and *Gip* were found to be highly expressed in Tomato-
263 positive cells of upper SI and lower SI (Fig. 5A and 5B). On the other hand, *Glp-1* was
264 expressed in I cells of upper SI and colon (Fig. 5C). These three gut hormones were not

265 expressed in Tomato-negative cells of SI and colon. These results indicate that some gut
266 hormone-producing cells overlap with I cells.

267

268 **Discussion**

269 In previous studies, characterization of I cells was done using purified cells from the
270 intestine of transgenic (CCK-GFP Tg) mice expressing green fluorescence protein (GFP)
271 under control of a *Cck* promoter derived from a BAC clone (Liou *et al.* 2011). Although
272 expression of some molecules associated with nutrient sensing in I cells has been
273 reported, these analyses focused on I cells expressed in small intestine. We have
274 established CCK-Tomato mice in which Tomato is expressed under endogenous and native
275 *Cck* promoter; the present study is the first to report I cell number and the expression of
276 CCK and various molecules associated with nutrient sensing in I cells of each part of the GI
277 tract.

278 I cells in the GI tract have previously been evaluated by immunohistochemistry with
279 anti-CCK antibodies. I cells are distributed throughout the small intestine and large intestine,
280 but the number of I cells in the small intestine is greater (Fakhry *et al.* 2017). Our findings
281 regarding I cell number in the GI tract of CCK-Tomato mice by immunohistochemistry with
282 anti-RFP antibodies are consistent with previous studies. However, CCK-Tomato mice
283 enabled evaluation of not only I cell number in the GI tract, but also *Cck* gene expression in
284 isolated I cells. Using the flow cytometry system, I cells among epithelial cells of upper SI,
285 lower SI, and colon were found to occur at the rate of $0.95 \pm 0.30\%$, $0.54 \pm 0.14\%$, and 0.06

286 $\pm 0.01\%$, respectively. A majority of the I cells were detected in upper SI, and their frequency
287 decreased toward the distal part of the GI tract. The expression levels of *Cck* mRNA in
288 isolated I cells from upper SI were highest in the GI tract, and decreased toward the distal
289 part of the GI tract. These results indicate that I cells in upper SI are the main contributor to
290 CCK secretion in response to various nutrients.

291 Fat ingestion strongly stimulates CCK secretion (Green *et al.* 1989). GPR40, GPR120,
292 and GPR119 are receptors activated by the nutrients LCFAs and OEA. These receptors are
293 reported to be expressed in incretin-producing cells and to be involved in incretin secretion
294 (Iwasaki *et al.* 2015, Sankoda *et al.* 2019). Bile, which is composed of bile acids, is important
295 for fat digestion and absorption, and is reported to induce CCK secretion in the fasting state
296 (Meyer-Gerspach *et al.* 2013). TGR5, a bile acid receptor, is expressed in L cells and is
297 involved in GLP-1 secretion (Brighton *et al.* 2015). Previous studies using the mouse
298 intestinal cell line STC-1 and *GPR40*- or *GPR120*-knockout mice showed that GPR40 and
299 GPR120 are involved in CCK secretion in response to LCFAs and fat (Tanaka *et al.* 2008,
300 Sankoda *et al.* 2017). On the other hand, it remains unclear whether GPR119 and TGR5 are
301 involved in CCK secretion, although these receptors are expressed in I cells of the small
302 intestine of CCK-GFP Tg mice (Sykaras *et al.* 2012). In our study, *Gpr40*, *Gpr120*, and *Gpr119*
303 were found to be expressed mainly in Tomato-positive cells of upper and lower SI and were
304 not detected in the cells of colon. *Tgr5* was highly expressed in Tomato-positive cells of
305 lower SI. These results indicate that these receptors may well be involved in CCK secretion
306 upon fat ingestion. Indeed, some LCFA transporters are expressed in various tissues

307 including intestine. We evaluated gene expression of *Fatp1-5* and *Cd36* mRNA in Tomato-
308 positive cells and -negative cells, and found that *Fatp4* and *Cd36* are expressed in Tomato-
309 positive cells as well as -negative cells. Our data is consistent with the previous report
310 showing that FATP4 and CD36 are involved in GLP-1 and CCK secretion, respectively (Poreba
311 *et al.* 2012, Sundaresan *et al.* 2013), and go further to suggest their role in CCK secretion
312 upon fat ingestion.

313 Glucose and fructose are known to induce CCK secretion (Kuhre *et al.* 2014); the
314 glucose transporters SGLT1 and GLUT2 and fructose transporter GLUT5 are expressed in
315 enteroendocrine cells and are involved in glucose and fructose-induced gut hormone
316 secretion, respectively (Reimann *et al.* 2008, Parker *et al.* 2009, Mace *et al.* 2012, Gorboulev
317 *et al.* 2012). The previous study using small intestine of CCK-GFP Tg mice revealed that
318 SGLT1 is expressed in I cells as well as other intestinal epithelial cells (Kaelberer *et al.* 2018),
319 but the expression of GLUT2 and GLUT5 in I cells was not examined. In the present study,
320 *Sglt1*, *Glut2*, and *Glut5* were found to be expressed in both Tomato-positive cells and -
321 negative cells in upper SI, lower SI, and colon, and the expression levels tended to be higher
322 in upper SI than those in lower SI and colon. These results revealed that the expression
323 patterns in Tomato-positive and -negative cells in SI and colon are similar among the three
324 transporters.

325 Peptide transporter PEPT1, peptone receptor GPR93, and amino acid-sensing
326 receptor CASR have been identified as protein metabolite-sensing molecules associated
327 with gut hormone secretion (Feng *et al.* 2010, Mace *et al.* 2012, Diakogiannaki *et al.* 2013).

328 *In vitro* and *in vivo* studies have shown that GPR93 and CASR are involved in amino acid-
329 induced CCK secretion from I cells (Choi *et al.* 2007, Liou *et al.* 2011); PEPT1, GPR93, and
330 CASR have been reported to be expressed in I cells of small intestine of CCK-GFP Tg mice
331 (Liou *et al.* 2011). In the present study, these molecules were found to be expressed in
332 Tomato-positive cells of upper and lower SI; *Pept1* and *Gpr93* were found to be expressed
333 in both Tomato-positive and -negative cells. On the other hand, *Casr* was expressed in
334 Tomato-positive cells but not in Tomato-negative cells, indicating that *Casr* is specifically
335 expressed in I cells. In colon, expression levels of *Pept1* mRNA were significantly higher in
336 Tomato-negative cells than those in Tomato-positive cells. As PEPT1 is reported to play an
337 important role in the regulation of water absorption into intestinal epithelium (Wuensch *et*
338 *al.* 2013), the molecule might be highly expressed in intestinal epithelial cells detected as
339 Tomato-negative cells.

340 CCK plays a key physiological role in fat absorption and regulation of energy intake.
341 Thus, regulation of nutrient-sensing molecule-mediated CCK secretion might represent
342 possible novel therapeutic approaches to obesity and type 2 diabetes. Analysis using CCK-
343 Tomato mice revealed that I cells are broadly distributed throughout the GI tract, and that
344 the various molecules involved in nutrient sensing are abundantly expressed in I cells.

345

346 **Declaration of interests**

347 N. I. received joint research grants from Daiichi Sankyo Co., Ltd., Terumo Co., Ltd., and
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352 Daiichi Sankyo Co., Ltd., Mitsubishi Tanabe Pharma Co., Ltd., Takeda Pharmaceutical Co., Ltd.,
353 Japan Tobacco Inc., Kyowa Kirin Co., Ltd., Sumitomo Dainippon Pharma Co., Ltd., Astellas
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360 **Author contribution statement**

361 T.K. and N.H. planned the study, researched data, contributed to discussion, wrote, reviewed
362 and edited the manuscript. E.I-O., A.S., T.H., X.L., T.Y., and S.Y. researched data. N.I. planned
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550

551 **Figure legends**

552 **Figure 1. Phenotype of CCK-Tomato mice**

553 (A) Body weight, (B) food consumption, (C) energy expenditure, and locomotor activity
554 (n=5-6). Blood glucose levels and plasma insulin and CCK levels during (D) OGTTs and (E)
555 OCTTs (n=6). Control mice (white circles) and CCK-Tomato mice (black circles). #P<0.05,
556 ##P<0.01 vs plasma glucose levels at 0 min, n.s.; not significant.

557

558 **Figure 2. Localization of I cells in the GI tract of CCK-Tomato mice.**

559 (A) Immunohistochemical images of the upper SI, lower SI, and colon in CCK-Tomato mice.
560 Red: Tomato-expressing cells, Green: CCK-expressing cells, Yellow: merged image. (B)
561 Length of villus and (C) number of Tomato-expressing cells in 50 villi and crypts were
562 measured by immunohistochemistry (n=6). (D) Tomato-expressing cells were quantified as
563 the number of Tomato-expressing cells / length of mucous membrane (n=6). (E) The levels
564 of red fluorescence in isolated epithelial cells were evaluated and Tomato-positive cells
565 were counted from the data of flow cytometry analysis (n=6). (F) Expression of *Cck* mRNA
566 in I cells (n=6-7). #P<0.05 and ##P<0.01 vs. Tomato negative cells, *P<0.05, n.s.; not
567 significant.

568

569 **Figure 3. Expressions of FFARs and TGR5 mRNA and in I cells.**

570 Data are shown as relative expression to that of *Ppia* expression in parallel in the same
571 samples (A: *Gpr120*, B: *Gpr40*, C: *Gpr119*, D: *Gpr43*, E: *Gpr41*, F: *Tgr5*) (n=6-8). #P<0.05 and
572 ##P<0.01 vs. Tomato-negative cells, *P<0.05 and **P<0.01, n.s.; not significant.

573

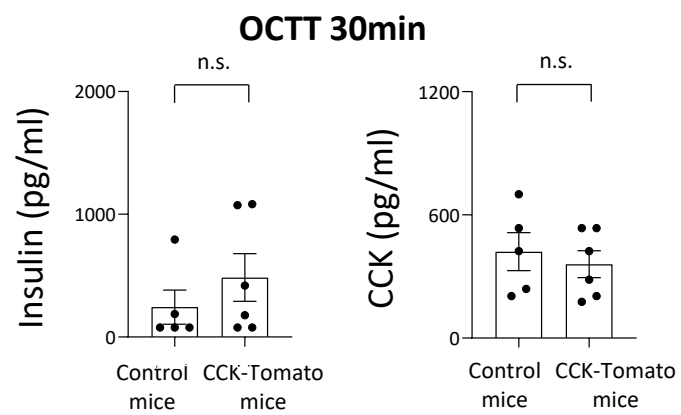
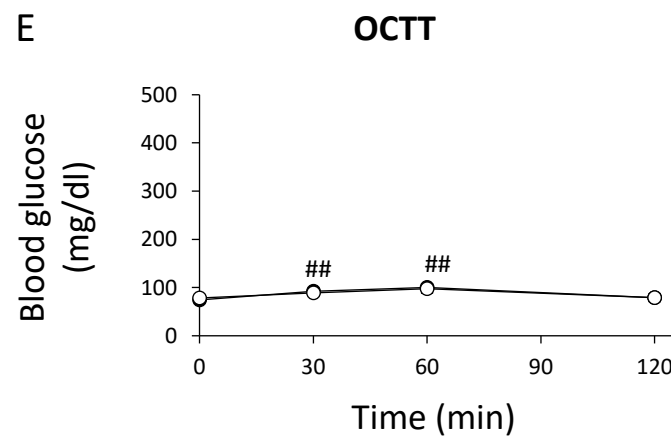
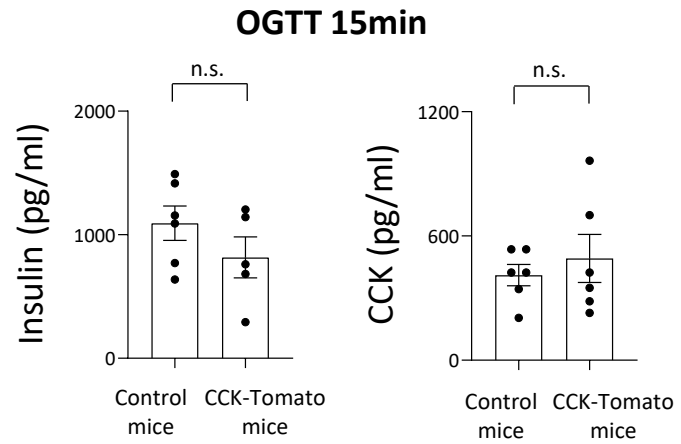
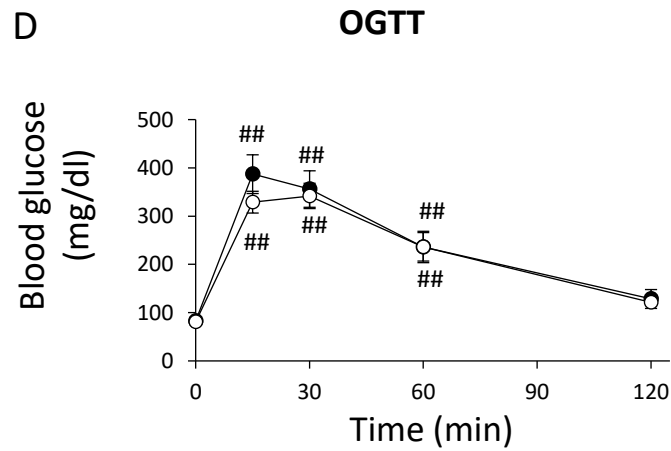
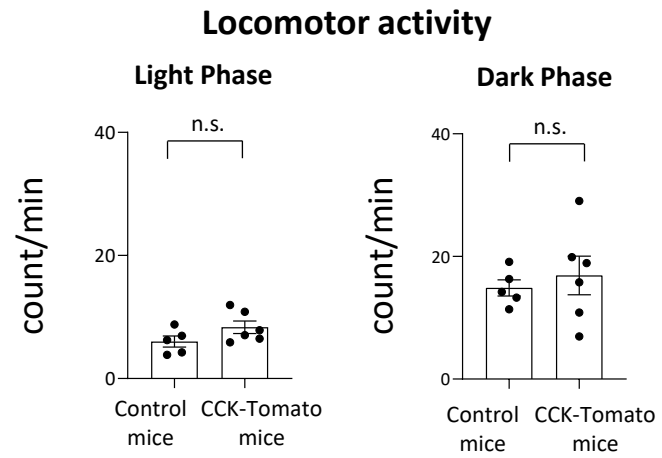
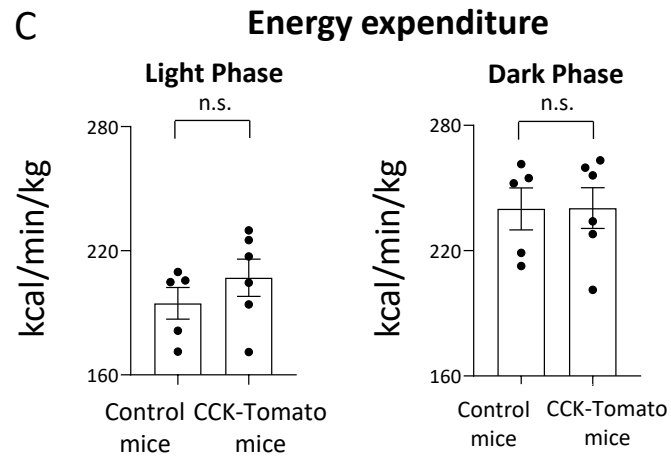
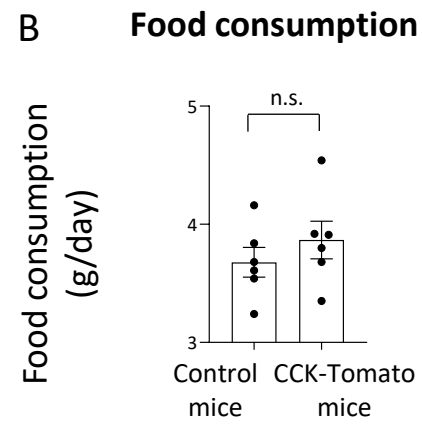
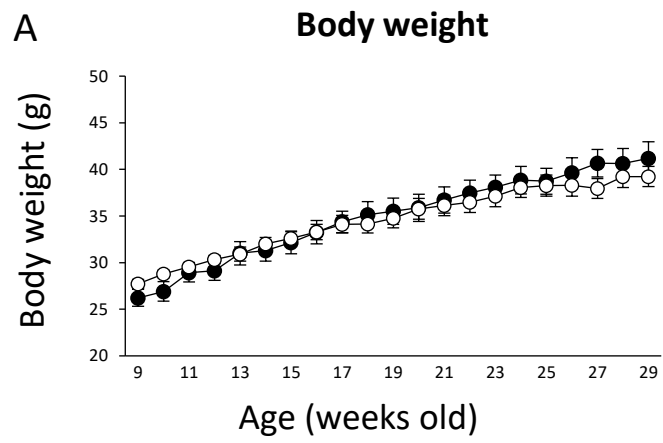
574 **Figure 4. Expressions of glucose transporters, amino acid transporter, and amino acid**
575 **receptors mRNA in I cells.**

576 Data are shown as relative expression to that of PPIA expression in parallel in the same
577 samples (A: *Sglt1*, B: *Glut2*, C: *Glut5*, D: *Pept1*, E: *Gpr93*, F: *Casr*) (n=6-8). #P<0.05 and
578 ##P<0.01 vs. Tomato-negative cells, *P<0.05 and **P<0.01, n.s.; not significant.

579

580 **Figure 5. Expressions of gut hormones mRNA in I cells.**

581 Expression levels of (A) *Secretin* mRNA, (B) *Gip* mRNA, and (C) *Glp-1* mRNA in Tomato-
582 positive and -negative cells. Data are shown as relative expression to that of PPIA expression
583 in parallel in the same samples (n=6-8). #P<0.05 and ##P<0.01 vs. Tomato-negative cells,
584 *P<0.05 and **P<0.01, n.s.; not significant.



○ Control mice ● CCK-Tomato mice

